

What is claimed is:

1. A nucleic acid array comprising a plurality of immobilized elements in an array at addressible locations on a substrate, wherein the plurality of elements comprises
5 nucleic acid sequences from a chromosome syntenic strand, and a first set of the elements are from a first species of organism and a second set of the elements are from a second species and the first species and second species are different, and wherein the nucleic acids in the elements from the first species of organism comprise nucleic acid sequences that are homologous to nucleic acid sequences in nucleic acid elements from a syntenic chromosome
10 of the second species of organism.
2. The array according to claim 1, wherein the nucleic acid in the first and set set of elements is cloned genomic DNA.
3. The array according to claim 2, wherein the cloned genomic DNA is carried on a vector selected from the group of vectors consisting of yeast artificial chromosomes
15 (YACs), bacterial artificial chromosomes (BACs), mammalian artificial chromosomes (MACs), and phage P1 artificial chromosomes (PACs).
4. The array according to any of claims 1-3, wherein at least one organism is selected from the group consisting of rodents, non-human primates, marine mammals, lagomorphs, porcines, bovines, carnivores, caprines, equines, amphibia, fish, and insects.
- 20 5. The array according to any of claims 1-3, wherein at least one organism is a non human transgenic mammal or a mammal having a model disease.
6. The array according to any of claims 1-3, wherein at least one organism is a human.
7. The array according to any of claims 1-3, wherein at least one organism is
25 selected from the group consisting of a gorilla, a chimpanzee, a monkey, a dog, a hamster, a mouse, a rat, a rabbit, a guinea pig, a sheep, a goat, a swine, a cow, a horse, a frog, a toad, a zebra fish, and a fly.
8. The array according to any of claims 1-3, wherein the species of organism are human and mouse.
- 30 9. The array according to any of claims 1-8, wherein the array further comprises a multi-array surface comprising a plurality of non-contiguous arrays, each array comprising the nucleic acid elements of the first set and the nucleic acid elements of the second set.

10. The array according to any of claims 1-9, wherein at least one element of nucleic acid of the first species is at least about 50% homologous to at least one element of nucleic acid of the second species.
11. The array according to any of claims 1-10, wherein at least one element of
5 nucleic acid of the first species is at least about 70% homologous to at least one element of nucleic acid of the second species.
12. The array according to any of claims 1-11, wherein at least one element of nucleic acid of the first species is at least about 90% homologous to at least one element of nucleic acid of the second species.
- 10 13. The array according to any of claims 1-12, wherein the contains at least one calibration spot.
14. The array according to any of claims 1-13, wherein the elements comprise nucleic acid sequences representing at least one chromosome of at least one species.
15. The array according to any of claims 1-14, wherein the elements comprise
15 nucleic acid sequences representating a genome of at least one of the species.
16. The array according to any of claims 9-15, wherein each of the plurality of non-contiguous arrays is separated from another of the arrays by a barrier.
17. A method of measuring genotoxicity of a composition or a physical force in an environment to a cell of a species of organism, the method comprising
20 contacting a test cell or a cell population of a first species with the composition or force;
obtaining a sample of nucleic acid from the contacted test cell or population; and
analyzing the nucleic acid of the sample for abnormalities by hybridizing the nucleic acid to an array of syntenic nucleic acid immobilized at addressible locations on a substrate,
25 the syntenic array having elements comprising sequences of syntenic nucleic acid from the genome of the first species, and having elements of sequences of syntenic nucleic acid from the genome of at least a second species of organism.
18. The method according to claim 17, wherein the second species is a human.
19. The method according to either of claims 17-18, wherein contacting is adding
30 the composition to the cell or the population, or exposing the cell or the population to the force, wherein the cell or population is in a cell culture.
20. The method according to either of claims 17-18, wherein the test cell or population is an organism of the first species in vivo.

21. The method according to either of claims 17-18, wherein treating the cell or organism in vivo is administering the composition by a route selected from the group of administering orally, topically, transdermally, injecting, or is exposing the cell or organism to the force.

5 22. The method according to any of claims 18-18 and claim 20, wherein contacting the first species in vivo is exposing the organism to the composition or the force in a natural environment.

23. The method according to any of claims 17-22, wherein the first species is selected from the group consisting of gorilla, chimpanzee, monkey, dog, hamster, mouse, rat, 10 rabbit, guinea pig, sheep, goat, swine, cow, horse, frog, toad, fish, and insect.

24. The method according to any of claims 17-23, wherein analyzing the genome of the contacted organism further comprises comparing hybridization of a sample of nucleic acid from the test cell to the array, with hybridization of a sample of nucleic acid from a reference cell to the array.

15 25. The method according to any of claims 17-24, wherein the reference cell is a cell from any of the first, second or third species.

26. The method according to any of claims 17-24, wherein the first species is a transgenic non-human mammal or a mammal having a model disease.

20 27. The method according to claim any of claims 17-25, wherein the reference cell is a cell of the first species not administered the composition and is otherwise identical to the test cell.

28. The method according to any of claims 17-27, further comprising comparing hybridization of nucleic acid from the test cell to the array and hybridization of nucleic acid from the reference cell to the array with hybridization of each to a calibration spot.

25 29. The method according to any of claims 17-28, further comprising prior to hybridizing, labeling separately each of the test cell nucleic acid and the reference cell nucleic acid with a first fluorescent dye and a second fluorescent dye, wherein the first dye and the second dye have different emission spectra.

30 30. The method according to claim any of claims 17-29, further comprising after labeling, preparing a first mixture comprising the test cell nucleic acid labeled with the first dye and the reference cell nucleic acid labeled with the second dye, and preparing a second mixture comprising the test cell nucleic acid labeled with the second dye and the reference cell nucleic acid labeled with the first dye, and separately hybridizing each of the first mixture and the second mixture to iterations of the syntenic array.

31. The method according to any of claims 17-30, wherein the iterations of the syntenic array are a multi-array surface comprising a plurality of non-contiguous syntenic arrays, and hybridizing the mixtures to the array is separately applying each of the first and second mixtures to a member of the plurality of syntenic arrays.

5 32. The method according to any of claims 17-31, further comprising comparing the genome of the test cell and the reference cell by normalizing a ratio of extent of hybridization of the first and second dyes to each element for each of the first and second mixtures.

10 33. The method according to any of claims 17-32, further comprising plotting the resulting set of ratios as a function of the location of each of the nucleic acids as a distance along a chromosome from the p-terminus to the q-terminus, to obtain a representation of the test cell chromosome.

15 34. The method according to any of claims 31-33, wherein hybridizing the first mixture and the second mixture to iterations of the syntenic array on the multi-array surface further comprises at least one of separately applying cover to each of the mixtures, applying the mixtures to areas separated by barriers, and adding a viscosity-increasing solute to each of the mixtures.

35. The method of any of claims 17-34, further comprising identifying a chromosome and a chromosomal location of a chromosomal abnormality of the test organism.

20 36. The method according to any of claims 17-35, wherein the first species is non-human, the syntenic array comprises elements of the human genome, and the method further comprises determining an homologous chromosome and chromosomal location of the abnormality in the human genome.

25 37. The method according to claim 36, wherein the nucleic acid of the elements immobilized in the array on the substrate comprises cloned DNA.

38. The method according to claim 36, wherein an amount of chromosomal abnormalities in the test sample nucleic acid compared to the reference sample nucleic acid is an indication of an extent of genotoxicity of the composition or the force.

30 39. The method according to any of claims 17-38, wherein the composition or force is selected from the group consisting of: a hazardous occupational compound, a chemical weapon, airborne dust, photochemical smog, a natural product, a cosmetic, a food additive, an agricultural product, an industrial compound, a new chemical entity, a lead compound, a pharmaceutical product, sewage, and an environmental sample, and an extract or

preparation thereof, an emission from a radioactive material, an ultra-violet beam, and an X-ray beam.

40. The method according to any of claims 30-39, wherein each of the iterations on the multi-array surface further comprises at least one calibration spot.

5 41. The method according to either of claims 28 and 40, wherein the calibration spot comprises nucleic acid sequences from a plurality of elements in the array.

42. A kit for use of the method according to any of claim 17-41, comprising at least one syntenic array having nucleic acid elements with nucleotide sequences from genomes of a plurality of species of organism immobilized on a surface, and a container.

10 43. The kit according to claim 42, further comprising a plurality of detectable labels, and instructions for use.

44. The kit according to either of claims 42-43, wherein the at least one syntenic array comprises a multi-array surface having a plurality of syntenic arrays.

45. A method of identifying the presence and location of a chromosomal
15 abnormality in cells of a subject during progression of a disease, the method comprising obtaining a nucleic acid sample from the cells affected by the disease; and analyzing the sample for chromosomal abnormalities by hybridizing the sample to elements of a first syntenic nucleic acid array having nucleic acid from the genome of a first species, and further hybridizing the sample to elements of a second syntenic nucleic acid
20 array having nucleic acid from the genome of a second species, the elements of the first and second arrays being immobilized on a substrate.

46. The method according to claim 45, wherein the first species or second species is human.

25 47. The method according to either of claims 45-46, wherein the disease is an animal model of a human disease.

48. The method according to any of claims 45-47, wherein the disease is a cancer.

49. The method according to any of claims 45-48, wherein the disease is a solid tumor or a blood proliferative condition.

30 50. The method according to any of claims 45-49, wherein the disease is selected from the group of cancers of skin, lung, breast, head and neck, prostate, ovary, brain, leukemia, gastric, stomach, esophagous, pancreas, and lymphoma.

51. The method according to any of claims 45-50, wherein the disease is a stage I cancer.

52. The method according to any of claims 45-50, wherein the cancer is selected from stage II, III and IV cancers.

53. The method according to any of claims 45-50, wherein the cancer is metastatic.

5 54. The method according to any of claims 45-53, further comprising obtaining an additional nucleic acid sample of cells from the subject at a time point representing a different stage of progression of the disease.

55. The method according to any of claims 45-54, wherein the disease is selected from the group of animal cancers consisting of lung cancer, mesothelioma, adenocarcinoma,
10 and prostate cancer.

56. The method according to any of claims 45-55, wherein the substrate comprises a multi-array surface having a plurality of syntenic arrays, the arrays comprising nucleic acid elements of the first species and nucleic acid elements of the second species.

57. The method according to any of claims 45-56, wherein the substrate further
15 includes at least one calibration spot comprising nucleic acid elements from a plurality of elements of the array.